Claim Amendments:

1. - 25. (cancelled)

26. A process for making compounds of the formula 1:

$$R_{3}$$
 R_{4} $R_{7} = H \text{ or } R_{7} = H \text{ or } R_{1}$ R_{1} R_{1} R_{1} R_{1} R_{2} R_{3} R_{4} $R_{7} = H \text{ or } R_{1}$ R_{1} R_{2} R_{3} R_{4} R_{5} R_{7} R_{8} $R_{10} = OH \text{ or } R_{10}$ $R_{10} = OH \text{ or } R_{12}$

wherein:

 R_1 is H or OH; R_2 - R_4 are each independently H, CH₃, or CH₂CH₃; R_5 is H or OH; and R_6 is H, CH₃, or CH₂CH₃; R_7 is H or desosamine; R_8 is H, CH₃, or CH₂CH₃; R_9 is OH, mycarose (R_{12} is H), or cladinose (R_{12} is CH₃), R_{10} is H; or $R_9 = R_{10} = O$; and R_{11} is H, CH₃, or CH₂CH₃

27. A process for the production of compounds of formula 1

$$R_{3}$$
 R_{4}
 $R_{7} = H \text{ or } R_{7} = H \text{$

and to pharmaceutically acceptable salts thereof, wherein:

 R_1 is H or OH; R_2 - R_4 are each independently H, CH₃, or CH₂CH₃; R_5 is H or OH; and R_6 is H, CH₃, or CH₂CH₃; R_7 is H or desosamine; R_8 is H, CH₃, or CH₂CH₃; R_9 is OH, mycarose (R_{12} is H), or cladinose (R_{12} is CH₃), R_{10} is H; or $R_9 = R_{10} = O$; and R_{11} is H, CH₃, or CH₂CH₃, with the proviso that when R_2 - R_4 are CH₃, R_6 is CH₃, R_8 is CH₃, and R_{11} is CH₃, then R_1 and R_5 are not H and R_{12} is not H; or also when R_2 - R_4 are CH₃, R_6 is CH₃, R_8 is CH₃, and R_{11} is CH₃, then R_1 and R_5 are not OH and R_{12} is not H; said process comprising culturing a transformant organism which contains a DNA gene assembly which produces a 14-membered macrolide, said gene assembly comprising a loading module of the form KSq-ATq-ACP where:

- a) KSq represents a domain operative to decarboxylate a malonate substrate carried by the ACP
- b) ATq represents an acyltransferase domain operative to load selectively a malonate unit onto the ACP; and
- c) ACP represents an acyl carrier protein and a plurality of extension modules, wherein said extension modules are not usually associated with a loading module that effects decarboxylation of a malonyl residue.
- 28. The process of claim 27, wherein the loading module is selected from the oleandomycin, spiramycin, niddamycin, methymycin or monensin PKSs.
- 29. The process of claim 27, wherein the plurality of extension modules correspond to the extension modules of the erythromycin PKS.
- 30. The process of claim 28, wherein the plurality of extension modules correspond to the extension modules of the erythromycin PKS.
- 31. The process of claim 27, wherein the organism is selected from the group consisting of: Saccharopolyspora erythraea, Streptomyces coelicolor, Streptomyces avermitilis, Streptomyces griseofuscus, Streptomyces cinnamonensis, Streptomyces fradiae, Streptomyces longisporoflavus, Streptomyces hygroscopicus, Micromonospora griseorubida, Streptomyces lasaliensis, Streptomyces venezuelae, Streptomyces antibioticus, Streptomyces lividans, Streptomyces rimosus, Streptomyces albus, Amycolatopsis mediterranei, and Streptomyces tsukubaensis.

- 32. The process of claim 28, wherein the organism is selected from the group consisting of: Saccharopolyspora erythraea, Streptomyces coelicolor, Streptomyces avermitilis, Streptomyces griseofuscus, Streptomyces cinnamonensis, Streptomyces fradiae, Streptomyces longisporoflavus, Streptomyces hygroscopicus, Micromonospora griseorubida, Streptomyces lasaliensis, Streptomyces venezuelae, Streptomyces antibioticus, Streptomyces lividans, Streptomyces rimosus, Streptomyces albus, Amycolatopsis mediterranei, and Streptomyces tsukubaensis.
- 33. The process of claim 29, wherein the organism is selected from the group consisting of: Saccharopolyspora erythraea, Streptomyces coelicolor, Streptomyces avermitilis, Streptomyces griseofuscus, Streptomyces cinnamonensis, Streptomyces fradiae, Streptomyces longisporoflavus, Streptomyces hygroscopicus, Micromonospora griseorubida, Streptomyces lasaliensis, Streptomyces venezuelae, Streptomyces antibioticus, Streptomyces lividans, Streptomyces rimosus, Streptomyces albus, Amycolatopsis mediterranei, and Streptomyces tsukubaensis.
- 34. The process of claim 30, wherein the organism is selected from the group consisting of: Saccharopolyspora erythraea, Streptomyces coelicolor, Streptomyces avermitilis, Streptomyces griseofuscus, Streptomyces cinnamonensis, Streptomyces fradiae, Streptomyces longisporoflavus, Streptomyces hygroscopicus, Micromonospora griseorubida, Streptomyces lasaliensis, Streptomyces venezuelae, Streptomyces antibioticus, Streptomyces lividans, Streptomyces rimosus, Streptomyces albus, Amycolatopsis mediterranei, and Streptomyces tsukubaensis.
- 35. The process of claim 27, which additionally comprises recovering a compound of formula 1.